

2.13.2K	GACATCCAGA	TGACCCAGTT	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50			
A30	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50			
2.14.3K	-----	-----	----TCCTCC	CTGTC	TGCAT	CTGTAGGAGA	26			
2.12.1K	-----	-----	-----	-----	TGCAT	CTGTAGGAGA	15			
4.9.2K	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50			
Consensus	GACATCCAGA	TGACCCAGTY	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50			
CDR1										
2.13.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AA	TGATTTAG	100			
A30	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AA	TGATTTAG	100			
2.14.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	CG	TGATTTAG	76			
2.12.1K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	CG	TGATTTAG	65			
4.9.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AG	TGATTTAG	100			
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	MR	TGATTTAG	100			
CDR2										
2.13.2K	GCTGGT	TCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150			
A30	GCTGGT	TCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150			
2.14.3K	GCTGGT	TCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	126			
2.12.1K	GCTGGT	TCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	115			
4.9.2K	GCTGGT	TCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150			
Consensus	GCTGGT	TCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150			
CDR3										
2.13.2K	GCATCC	GTT	TCA	AGG	GGTCCC	ATCA	AGGTT	CAGCG	GCAGTGGATC	200
A30	GCATCC	GTT	TCA	AGG	GGTCCC	ATCA	AGGTT	CAGCG	GCAGTGGATC	200
2.14.3K	GCATCC	GTT	TCA	AGG	GGTCCC	ATCA	AGGTT	CAGCG	GCAGTGGATC	176
2.12.1K	GCATCC	GTT	TCA	AGG	GGTCCC	ATCA	AGGTT	CAGCG	GCAGTGGATC	165
4.9.2K	GCATCC	AAAT	TCA	AGG	GGTCCC	ATCA	AGGTT	CAGCG	GCAGTGGATC	200
Consensus	GCATCC	AAWT	TCA	AGG	GGTCCC	ATCA	AGGTT	CAGCG	GCAGTGGATC	200
CDR4										
2.13.2K	TGGGACAGAA	TTC	ACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250			
A30	TGGGACAGAA	TTC	ACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250			
2.14.3K	TGGGACAGAA	TTC	ACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	226			
2.12.1K	TGGGACAGAA	TTC	ACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	215			
4.9.2K	TGGGACAGAA	TTC	ACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250			
Consensus	TGGGACAGAA	TTC	ACTCTCA	CAATCAGCG	CCTGCAGCCT	GAAGATTTTG	250			
CDR5										
2.13.2K	CAACTTATTA	CTGT	TACAA	CATAA	TAGTT	AC	CGTGCAG	TTTT	TGGCCAG	300
A30	CAACTTATTA	CTGT	TACAG	CATAA	TAGTT	AC	CC-TCCN-	-----		28E
2.14.3K	CAACTTATTA	CTGT	TACAG	CATAA	TAGTT	AT	CTCGGAC	GT	TCGGCCAA	276
2.12.1K	CAACTTATTA	CTGT	TACAG	CATAA	TAGTT	AT	CTCGGAC	GT	TCGGCCAA	265
4.9.2K	CAACTTATTA	CTGT	TACAG	CATAA	TAGTT	AC	CTCTCAC	TT	TCGGCGGA	300
Consensus	CAACTTATTA	CTGT	TACAA	CATAA	TAGTT	AT	CTCYEENS	KT	TYGGCSRR	300
CDR6										
2.13.2K	GGGACCAAGC	TGGAGATCAA	AC----							322
A30	-----	-----	-----							28E
2.14.3K	GGGACCGAGG	TGGAAATCAT	ACGAAC							302
2.12.1K	GGGACCGAGG	TGGAAATCAT	ACGAAC							291
4.9.2K	GGGACCAAGC	TGGAGATCAA	AC----							322
Consensus	GGGACCAAGC	TGGAAATCAW	ACGAAC							326

FIG. 1A

4.17.3K	-----	-----	-----	-----	AGGAGA	7
O12	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
CDR1						
4.17.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGT	ACCTTTTAA	57
O12	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGC	AGCTATTTAA	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGY	ASCTATTTAA	100
4.17.3K	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAACTCCT	GATCATGTT	107
O12	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAACTCCT	GATCATGCT	150
Consensus	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAACTCCT	GATCATGCT	150
CDR2						
4.17.3K	GCATCCAGTT	TCAAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	157
O12	GCATCCAGTT	TCAAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	200
Consensus	GCATCCAGTT	TCAAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	200
4.17.3K	TGGGACAGAT	TTCACCTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	207
O12	TGGGACAGAT	TTCACCTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
Consensus	TGGGACAGAT	TTCACCTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
CDR3						
4.17.3K	CAACTTACTA	CTGTCAACAG	AGTTACAGT	CCCCACTCAC	TTTCGGCGGA	257
O12	CAACTTACTA	CTGTCAACAG	AGTTACAGT	CCCC-TCC-	-----	286
Consensus	CAACTTACTA	CTGTCAACAG	AGTTACAGT	CCCCAYYCH	TTTCGGCGGA	300
4.17.3K	GGGACCAAGG	TGGAGATCAA	AC			279
O12	-----	-----	--			286
Consensus	GGGACCAAGG	TGGAGATCAA	AC			322

FIG. 1B

6.1.1K	-----	50
A27	GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA	50
Consensus	GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT CTCCAGGGGA	
	CDR1	
6.1.1K	AGAGCCACC CTCTCCTGTA GGGCCAGTCA GAGTGTTCGC GGCAGGTA	49
A27	AGAGCCACC CTCTCCTGTA GGGCCAGTCA GAGTGTTCGC GGCAGGTA	100
Consensus	AGAGCCACC CTCTCCTGTA GGGCCAGTCA GAGTGTTCGC GGCAGGTA	100
6.1.1K	TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT	99
A27	TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT	150
Consensus	TAGCCTGGTA CCAGCAGAAA CCTGGCCAGG CTCCCAGGCT CCTCATCTAT	150
	CDR2	
6.1.1K	GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG	149
A27	GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG	200
Consensus	GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA GTGGCAGTGG	200
6.1.1K	GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT	199
A27	GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT	250
Consensus	GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG CCTGAAGATT	250
	CDR3	
6.1.1K	TTGCAGTGT TTACTGTCAG CAGTATGGTA GTTCACCTCG NACGTTCCGGC	249
A27	TTGCAGTGT TTACTGTCAG CAGTATGGTA GTTCACCTCG -----	290
Consensus	TTGCAGTGT TTACTGTCAG CAGTATGGTA GTTCACCTCG NACGTTCCGGC	300
6.1.1K	CAAGGGACCA AGGTGGAAAT CAAAC	274
A27	-----	290
Consensus	CAAGGGACCA AGGTGGAAAT CAAAC	325

FIG. 1C

2.12.1H	-----	GGGAGGC	TTGGTCAAGC	CTGGA	GGTC	26	
DP35	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGA	GGGC	50
Consensus	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGA	GGGC	50
CDR1							
2.12.1H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	76
DP35	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTACA	100
Consensus	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	100
2.12.1H	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAA	TG	GGTTTCATAC	126
DP35	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAA	TG	GGTTTCATAC	150
Consensus	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAA	TG	GGTTTCATAC	150
CDR2							
2.12.1H	ATTAGTAGTA	GTGGTAGTAC	CAGAG	ACTAC	GCAGACTCTG	TGAAGGGCCG	176
DP35	ATTAGTAGTA	GTGGTAGTAC	CAGAG	ACTAC	GCAGACTCTG	TGAAGGGCCG	200
Consensus	ATTAGTAGTA	GTGGTAGTAC	CAGAG	ACTAC	GCAGACTCTG	TGAAGGGCCG	200
2.12.1H	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA	226	
DP35	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA	250	
Consensus	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA	250	
2.12.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA	276	
DP35	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA	296	
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA	300	
CDR3							
2.12.1H	GTGGAAACTA	CTTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	326	
DP35	GTGGAAACTA	CTTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	296	
Consensus	GTGGAAACTA	CTTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350	
2.12.1H	AGGGACCACG	GTCACCGTCT	CCTCAG			352	
DP35	AGGGACCACG	GTCACCGTCT	CCTCAG			296	
Consensus	AGGGACCACG	GTCACCGTCT	CCTCAG			376	

FIG. 2A

PF2-2.14.3H.DNA	-----	GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	30
VIV-4/4.35	CAGGTGCAGC TGCAGGAGTC	GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	50
Consensus	CAGGTGCAGC TGCAGGAGTC	GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	50
		CDR1	
PF2-2.14.3H.DNA	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	AAATTACTACT	80
VIV-4/4.35	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	AAATTACTACT	100
Consensus	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	AAATTACTACT	100
		CDR1	
PF2-2.14.3H.DNA	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT		130
VIV-4/4.35	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT		150
Consensus	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT		150
		CDR2	
PF2-2.14.3H.DNA	ATCTATACCA GTGGGAGGCC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		180
VIV-4/4.35	ATCTATACCA GTGGGAGGCC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		200
Consensus	ATCTATACCA GTGGGAGGCC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		200
PF2-2.14.3H.DNA	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACT		230
VIV-4/4.35	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACT		250
Consensus	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACT		250
PF2-2.14.3H.DNA	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTT		280
VIV-4/4.35	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTT		288
Consensus	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTT		300
		CDR3	
PF2-2.14.3H.DNA	GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGGGACCC TGGTCACCGT		330
VIV-4/4.35	-----	AGGAGT-----	294
Consensus	GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGGGACCC TGGTCACCGT		350
PF2-2.14.3H.DNA	CTCCTCAG		338
VIV-4/4.35	-----		294
Consensus	CTCCTCAG		358

FIG. 2B

6.1.1H	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
4.9.2H	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
DP47	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
2.13.2H	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
Consensus	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50

CDR1

6.1.1H	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
4.9.2H	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
DP47	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
2.13.2H	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
Consensus	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100

CDR1

CDR2

6.1.1H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
4.9.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
DP47	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
2.13.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
Consensus	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150

CDR2

6.1.1H	ATTACTGGGA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
4.9.2H	ATTACTGGGA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
DP47	ATTACTGGGA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
2.13.2H	ATTACTGGGA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
Consensus	ATTACTGGGA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200

6.1.1H	GTTCAACATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
4.9.2H	GTTCAACATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
DP47	GTTCAACATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
2.13.2H	GTTCAACATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
Consensus	GTTCAACATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250

CDR3

6.1.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTC--	298
4.9.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTG	300
DP47	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTC	296
2.13.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTT	300
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTK	300

CDR3-for 4.9.2 and 2.13.2

6.1.1H	-----	-----	-----	-----	-----C-	299
4.9.2H	GGCTACGGTG	ACTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGGCCA	350
DP47	-----	-----	-----	-----	-----	296
2.13.2H	GGCTGGTCCG	ACTCTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGGCCA	350
Consensus	GGCTRSKSYG	ACTYTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGGCCA	350

CDR3-for 6.1.1

6.1.1H	AGGGACTACG	GTGATTATGA	GTTGGTTCGA	CCCCTGGGGC	CAGGGAACCC	349
4.9.2H	AGGGACCAC-	-----	-----	-----	-----	359
DP47	-----	-----	-----	-----	-----	296
2.13.2H	AGGGACCAC-	-----	-----	-----	-----	359
Consensus	AGGGACYACG	GTGATTATGA	GTTGGTTCGA	CCCCTGGGGC	CAGGGAACCC	400

FIG. 2C-1

6.1.1H	TGGTCACCGT CTCCTCAG	367
4.9.2H	-GGTCACCGT CTCCTCAG	376
DP47	-----	296
2.13.2H	-GGTCACCGT CTCCTCAG	376
Consensus	TGGTCACCGT CTCCTCAG	418

FIG. 2C-2

4.17.3H	-----	CCCAGGA CTGGTGAAGC CTTCCGAGAC	27
DP71	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCCGAGAC		50
Consensus	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCCGAGAC		50
		CDR1	
4.17.3H	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT		77
DP71	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT		100
Consensus	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT		100
		CDR1	
4.17.3H	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT		127
DP71	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT		150
Consensus	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT		150
		CDR2	
4.17.3H	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		177
DP71	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		200
Consensus	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		200
		CDR3	
4.17.3H	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGTT		227
DP71	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGTT		250
Consensus	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGTT		250
		CDR3	
4.17.3H	CTGTGACCGC TGC GGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC		277
DP71	CTGTGACCGC TGC GGACACG GCCGTGTATT ACTGTGCCAG GA-----		289
Consensus	CTGTGACCGC TGC GGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC		300
		CDR3	
4.17.3H	AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GACACACGGT		327
DP71	-----	GA-----	293
Consensus	AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GACACACGGT		350
		CDR3	
4.17.3H	CACCGTCTCC TCAG		341
DP71	-----		293
Consensus	CACCGTCTCC TCAG		364

FIG. 2D

Clone	C domain mutations	FR mutation	CDR mutation	Change in Cys	Change in glycosylation
2.13.2 Heavy	0	3	8	0	0
2.13.2 Light	0	1	4	1 (CDR3)	0
2.12.2 Heavy	0	2	8	0	0
2.12.2 Light	0	3	5	0	0

FIG. 3A

PF2 2.13.2 Heavy chain (DP-47(3-23)/D6-19/JH6)

MEFGLSHLPL VAILKGVQCE VQLLESQGGGL VQPGGSLRLS CTASGFTFSS YAMNHRQAP GKGLEHVSAL SSGGCTTFYA DSVKGRFTIS RDNSRTTLXL
 MEFGLSHLPL VAILKGVQCE VQLLESQGGGL VQPGGSLRLS CAASGFTFSS YAMSHVRQAP GKGLEHVSAL SSGGSTYYA DSVKGRFTIS RDNSKNTLXL
 QKNSLRABDI AVYICAK--D LGHSDSYYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSHNSG ALTSGVHTFP
 QKNSLRABDI AVYICAKGYS SCH--YYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSHNSG ALTSGVHTFP
 VLQSSGLYS LSSVTVVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF
 VLQSSGLYS LSSVTVVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF
 NHYVDGVEVH NAKTKPREEQ FNSTFRVVSU LTVVHQDHLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
 NHYVDGVEVH NAKTKPREEQ FNSTFRVVSU LTVVHQDHLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
 DIAVEHESNG QPENNYKTP PMLDSGSGFF LYSKLTVDKS RHOQGNVFSC SVMHEALHNN YTKSLSLSP GK
 DIAVEHESNG QPENNYKTP PMLDSGSGFF LYSKLTVDKS RHOQGNVFSC SVMHEALHNN YTKSLSLSP GK

FIG. 3B

PF2 2.13.2 LC (A30/JK2) * . .
 +
 MONRVP AOL L G L L L L H P P G A R C D I Q M T Q P P S S L S A S V G D R V T I T C R A S Q I R N D L C W Y Q Q K P G K A P K R L I Y A A S R L H R G V P S R F S G S G S G T E P T L T I S S L
 MONRVP AOL L G L L L L H P P G A R C D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q I R N D L C W Y Q Q K P G K A P K R L I Y A A S S L Q S G V P S R F S G S G S G T E P T L T I S S L
 . .
 Q P E D F A T Y Y C L Q M N S Y P C S F G Q G T K L E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N F Y P R E A K V Q H K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
 Q P E D F A T Y Y C L Q M N S Y P Y T F G Q G T K L E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N F Y P R E A K V Q H K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T

PLSKADY EK HKVYACEVTH QGLSSPVTKS FNRGEC
 LTLSKADY EK HKVYACEVTH QGLSSPVTKS FNRGEC

FIG. 3C

PF2 2.12.1 Heavy chain (DP-35 (3-11) / D3-3 / JH6) . .
 +
 H E F G L S W V F L V A I I K G V Q C Q A Q L V E S G G L V K P G S L R L S C A A S G T F S D Y M S W I R Q A P G K G L E H V S Y I S S S G S T R D Y A D S V K G R F T I S R D N A K N S L Y L
 H E F G L S W V F L V A I I K G V Q C Q V Q L V E S G G L V K P G S L R L S C A A S G T F S D Y M S W I R Q A P G K G L E H V S Y I S S S G S T I Y Y A D S V K G R F T I S R D N A K N S L Y L

 +
 Q M N S L R A E D T A V Y I C V R - - D G V E T T F - Y Y Y Y Y G M D V M G C Q T T V T V S S A S T K G P S V F P L A P C S R S T S E S T A A L G C L V K D Y F P E P V T V S H N S G A L T S G V H T F
 Q M N S L R A E D T A V Y I C A R V L R F L E W L L Y Y Y Y Y G M D V M G C Q T T V T V S S A S T K G P S V F P L A P C S R S T S E S T A A L G C L V K D Y F P E P V T V S H N S G A L T S G V H T F
 P A V L Q S S G L Y S L S S V V T V P S S N F G T Q T Y T C N V D H K P S N T K V D K T V E R K C C V E C P P C P A P P V A G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V Q
 P A V L Q S S G L Y S L S S V V T V P S S N F G T Q T Y T C N V D H K P S N T K V D K T V E R K C C V E C P P C P A P P V A G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D P E V Q

 F N W Y V D G V E V H N A K T K P R E E Q F N S T F R V V S V L T V V H Q D W L N G K E Y K C K V S N K G L P A P I E K T I S K T K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P
 F N W Y V D G V E V H N A K T K P R E E Q F N S T F R V V S V L T V V H Q D W L N G K E Y K C K V S N K G L P A P I E K T I S K T K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P
 S D I A V E H E S N G Q P E N N Y K T P P M L D S D G S F F L Y S K L T V D K S R M Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K
 S D I A V E H E S N G Q P E N N Y K T P P M L D S D G S F F L Y S K L T V D K S R M Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K

FIG. 3D

PF2.12.1 Light chain (A30/Jx1)

MDMRVPAQLL	GLLLHFP	GA	RCDIQMTQSP	SSLSASVGDR	VTFTCRASQD	IRNDLGWYQQ	KPGKAPKRLI	YAAARLQSGV	P9RPSGSGSG	TEPTLTISL
MDMRVPAQLL	GLLLHFP	GA	RCDIQMTQSP	SSLSASVGDR	VTITCRASQD	IRNDLGWYQQ	KPGKAPKRLI	<u>YAAASLQSGV</u>	PSRPSGSGSG	TEPTLTISL
QPEDPATYYC	LQDNTPPTF		GQGTVEEIR	TVAAPSVFIF	PPSDEQLKSG	TASVVCLLNN	FYPREAKVQH	KVDNALQSGN	SQESVTEQDS	KDSTYSLSST
QPEDPATYYC	LQDNTPPTF		GQGTVEEIR	TVAAPSVFIF	PPSDEQLKSG	TASVVCLLNN	FYPREAKVQH	KVDNALQSGN	SQESVTEQDS	KDSTYSLSST
LTLSKADYEK	HKVYACEVTH		QGLSPVTKS	FNRGEC						
LTLSKADYEK	HKVYACEVTH		QGLSPVTKS	FNRGEC						

FIG. 3E

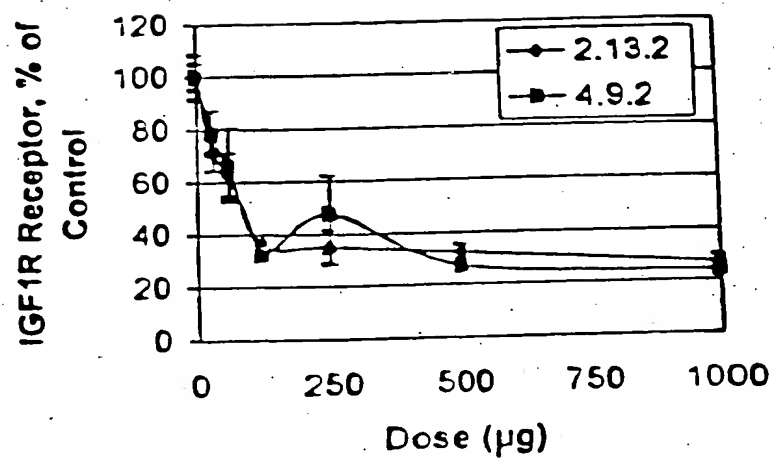


FIG. 4

Single Agent

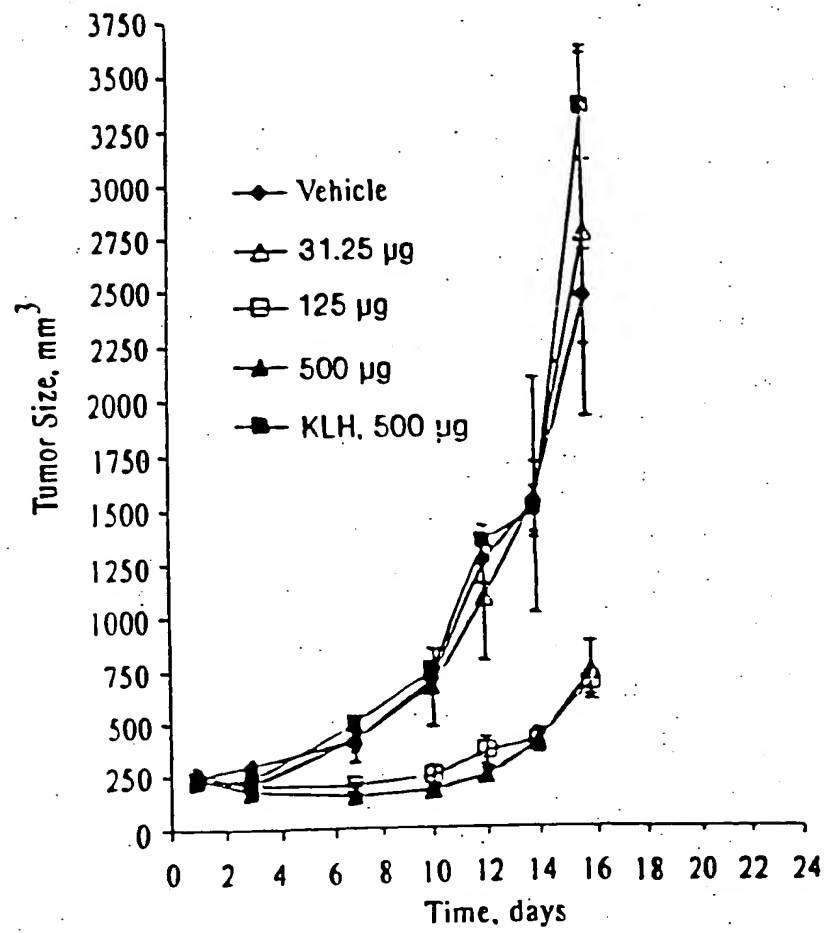


FIG. 5